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OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 21:10:37 ; Search time 787.52 Seconds

(without alignments)
9201.802 Million cell updates/sec

Title: US-09-988-971-1_COPY_694_942

Perfect score: 249
Sequence: 1 tggcgtatgagggcctgag.....aggccctggtgaccattac 249

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenBankl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
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9: gb_pr: *
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13: gb_vl: *
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30: em_hcg_hum: *
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32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rnd: *
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37: em_hcg_vrt: *
38: em_sy: *
39: em_hgo_hum: *
40: em_hgo_mus: *
41: em_hgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249	100.0	737	9	AF290986 Homo sapi
2	249	100.0	786	9	AF290985 Homo sapi
3	249	100.0	786	9	AF290986 Homo sapi
4	249	100.0	1183	6	AX443133 Sequence
5	249	100.0	1183	6	AX443133 Sequence
6	249	100.0	2415	9	AK025645 Homo sapi
7	249	100.0	2567	6	AX452880 Sequence
8	213.8	1348	10	AF287467	AF287467 Mus muscu
9	212.2	85.2	1321	10	AF434990 Mus muscu
10	150	60.2	145068	9	HS0197781
11	150	60.2	145833	2	AC026539
12	123.6	49.6	168498	2	AC125701
13	122.6	49.2	114096	2	AC123560
14	106.8	42.9	145833	2	AC026539
15	100.2	40.2	1926	9	HUMHCKB
16	100.2	40.2	2015	6	AX334501
17	100.2	40.2	2015	9	HUMHCKA
18	100.2	40.2	2044	9	BC014435
19	100.2	40.2	3701	5	CHRTCKL
20	100.2	39.8	4073	5	GRTKL
21	99.2	39.8	2105	9	AK026432
22	97	39.0	675	6	AR016398
23	97	39.0	675	6	AR019256
24	97	39.0	1491	9	AF228313
25	97	39.0	1515	9	MFA320181
26	97	39.0	1530	9	HSP120182
27	97	39.0	1589	9	HSU07236
28	97	39.0	2032	9	HSJCKB
29	97	39.0	2032	9	HUMHCKA
30	97	39.0	2129	9	HSU23852
31	97	39.0	2182	9	BC013200
32	96	38.6	2298	5	AF321110
33	95.4	38.3	1527	9	SSC277921
34	90.8	36.5	1533	6	E03080
35	90.8	36.5	2041	9	HSTCPTK
36	89	35.7	1911	6	AX401935
37	89	35.7	1911	10	RATHCTK
38	89	35.7	1911	10	S74141
39	89	35.7	1940	10	RRHCKR
40	89	35.7	2100	10	MUSLCK
41	89	35.7	2102	10	BC011474
42	89	35.7	2172	10	MMTKR
43	89	35.7	2200	10	RNFGR
44	87.6	35.2	2300	9	BC002836
45	87.6	35.2	2354	6	AX335936

ALIGNMENTS

RESULT 1
AF290986
LOCUS Homo sapiens Src-like adaptor protein-2 splice isoform mRNA,
DEFINITION complete cds.
ACCESSION AF290986
VERSION AF290986.1 GI:17351922
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 737)
AUTHORS Loreto, M.P. and McClade, C.J.
TITLE Direct Submission

Pred. No. is the number of results predicted by chance to have a

JOURNAL

Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

FEATURES

Location/Qualifiers

source

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/db_xref="taxon:9606"
/chromosome="20"
/tissue_type="thymus"
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/note="SLAP-2-V"
/codon_start=1
/product="Src-like adaptor protein-2 splice isoform"
/protein_id="AA13198.1"
/db_xref="GI:17351923"

CDS

/translation="MGSLPSRRKSLPSPLSSSVQGGPVTMEERKATVALGSPF
AGGPAELSLRGEPLTIVSEDDMTVLSEVSRVNIISVAVKSHGMVYGLSRE
KAEBLLPFGNGAFILRESQTRRGSYSLSRLSRPASMDIRHRYRHICLDNGMLYI
SPRLTPEPSIQALVDHYSEGMFAPMGQYPTPCACEDYTLERAGOLPPVF"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

280 TGGCTGTATGAGGGCTTGAGCAGAGGAGAAAGAGAGAACTGCTGTGTTTACCTGGGAC 339

Qy

61 CTTGAGAGGGGCTTCTCATCCGGAGAGCCAGACAGAGAGAGGCTTACTCTCTGTCA 120

Db

340 CTTGAGAGGGGCTTCTCATCCGGAGAGCCAGACAGAGAGAGGCTTACTCTCTGTCA 399

Qy

121 GTCCGCTTCAGCCGCTTCATCTTGAGACGGATCAGACATCAAGATCCACTGCTTT 180

Db

400 GTCCGCTTCAGCCGCTTCATCTTGAGACGGATCAGACATCAAGATCCACTGCTTT 459

Qy

181 GACATGCTGCTGTATCATCTCAGCCGCTCCTCCCTCACTCCAGAGCCCTGGTG 240

Db

460 GACATGCTGCTGTATCATCTCAGCCGCTCCTCCCTCACTCCAGAGCCCTGGTG 519

Qy

241 GACCATTCAC 249

Db

520 GACCATTCAC 528

RESULT 2

AF290985 786 bp mRNA linear PRI 22-APR-2002

LOCUS

Home sapiens Src-like adaptor protein-2 mRNA, complete cds.

ACCESSION

AF290985.1 GI:17351920

VERSION

AF290985.1 GI:17351920

KEYWORDS

Home sapiens.

SOURCE

Home sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 786)
Loreto, M.P. and McGrade, C.J.

AUTHORS

Direct Submission

TITLE

Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

JOURNAL

Location/Qualifiers

FEATURES

1..786
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/tissue_type="thymus"
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/note="SLAP-2"
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/product="Src-like adaptor protein-2"
/protein_id="AA13197.1"

CDS

/translation="MGSLPSRRKSLPSPLSSSVQGGPVTMEERKATVALGSPF
AGGPAELSLRGEPLTIVSEDDMTVLSEVSRVNIISVAVKSHGMVYGLSRE
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SPRLTPEPSIQALVDHYSEGMFAPMGQYPTPCACEDYTLERAGOLPPVF"

BASE COUNT

162 a 234 c 231 g 159 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

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Db

280 TGGCTGTATGAGGGCTTGAGCAGAGGAGAAAGAGAGAACTGCTGTGTTTACCTGGGAC 339

Qy

61 CTTGAGAGGGGCTTCTCATCCGGAGAGCCAGACAGAGAGAGGCTTACTCTCTGTCA 120

Db

340 CTTGAGAGGGGCTTCTCATCCGGAGAGCCAGACAGAGAGAGGCTTACTCTCTGTCA 399

Qy

121 GTCCGCTTCAGCCGCTTCATCTTGAGACGGATCAGACATCAAGATCCACTGCTTT 180

Db

400 GTCCGCTTCAGCCGCTTCATCTTGAGACGGATCAGACATCAAGATCCACTGCTTT 459

Qy

181 GACATGCTGCTGTATCATCTCAGCCGCTCCTCCCTCACTCCAGAGCCCTGGTG 240

Db

460 GACATGCTGCTGTATCATCTCAGCCGCTCCTCCCTCACTCCAGAGCCCTGGTG 519

Qy

241 GACCATTCAC 249

Db

520 GACCATTCAC 528

RESULT 3

AF26353 786 bp mRNA linear PRI 08-NOV-2001

LOCUS

Home sapiens Src-like adaptor protein-2 mRNA, complete cds.

ACCESSION

AF26353.1 GI:16797891

VERSION

AF26353.1 GI:16797891

KEYWORDS

Home sapiens.

SOURCE

Home sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 786)
Chen, P., Spencer, C., Fu, A. C., Sheng, N., Yu, P., Pali, E., Nagin, A.,
Shen, M., Yu, S., Chan, E., Wu, X., Li, C., Moisevich, M.,
Aversa, G., Kolbinger, F., Bennett, M. K., Mollinaux, S., Luo, Y.,
Payan, D. G., Mancebo, H. S. Y., and Wu, J.

AUTHORS

Functional Cloning of Src-like Adaptor Protein-2 (SLAP-2), a Novel
Inhibitor of Antigen Receptor Signaling

TITLE

J. Exp. Med. 194 (9), 1263-1276 (2001)

JOURNAL

Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
/chromosome="20"
1..786
/note="SLAP2; SH2 and SH3 domain-containing adaptor"
/codon_start=1
/product="Src-like adaptor protein-2"
/protein_id="AAU29204.1"

CDS

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AGGPAELSLRGEPLTIVSEDDMTVLSEVSRVNIISVAVKSHGMVYGLSRE
KAEBLLPFGNGAFILRESQTRRGSYSLSRLSRPASMDIRHRYRHICLDNGMLYI
SPRLTPEPSIQALVDHYSEGMFAPMGQYPTPCACEDYTLERAGOLPPVF"

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SPRLTFPLQALVDHYSELADICCLLEPEVJORAGPLPGKDIPLPVVQRTPLNWK
ELDSILFSEMAIGESBLLSEGRISLSEFYSINDEAVSLDDA"
BASE COUNT      162 a      234 c      231 g      159 t
ORIGIN
Query Match      100.0%; Score 249; DB 9; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTGATGAGGAGGCTTGAGCAGAGGAGAAAGCAGAGAACTGCTGTTGTTACTGGGAAC 60
DB 280 TGGCTGATGAGGAGGCTTGAGCAGAGGAGAAAGCAGAGAACTGCTGTTGTTACTGGGAAC 339
QY 61 CCGTGAAGGGGCTTCTCTCATCCGGAGAGCCACACAGAGAGGCTCTTACTCTGTCA 120
DB 340 CCGTGAAGGGGCTTCTCTCATCCGGAGAGCCACACAGAGAGGCTCTTACTCTGTCA 399
QY 121 GTCCGCTCAGCCGCTTGATCTTGAGACCGGATCAGACACTACAGATCCACTGCTT 180
DB 400 GTCCGCTCAGCCGCTTGATCTTGAGACCGGATCAGACACTACAGATCCACTGCTT 459
QY 181 GACAAATGGCTGCTGTAATCTTCAACCGCGCTCACTTCCCTCACTCCAGGCGCTGTG 240
DB 460 GACAAATGGCTGCTGTAATCTTCAACCGCGCTCACTTCCCTCACTCCAGGCGCTGTG 519
QY 241 GACCAATTAC 249
DB 520 GACCAATTAC 528

RESULT 4
AX443133
LOCUS      AX443133      1183 bp      DNA      linear      PAT 02-JUL-2002
DEFINITION      Sequence 74 from Patent WO0216599.
ACCESSION      AX443133
VERSION      AX443133.1 GI:21690555
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1
AUTHORS      Burgess,C.E., Conley,P.B., Grose,W.M., Hart,M., Kekuda,R.,
Shinkes,R.A., Spytek,K.A., Szekeres,E.S., Tomlinson,J.E.,
Topper,J.N. and Yang,R.B.
TITLE      Proteins and nucleic acids encoding same
JOURNAL      Patent: WO 0216599-A 74 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
FEATURES
source      1..1183
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Query Match      100.0%; Score 249; DB 6; Length 1183;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTGATGAGGAGGCTTGAGCAGAGGAGAAAGCAGAGAACTGCTGTTGTTACTGGGAAC 60
DB 677 TGGCTGATGAGGAGGCTTGAGCAGAGGAGAAAGCAGAGAACTGCTGTTGTTACTGGGAAC 736
QY 61 CCGTGAAGGGGCTTCTCTCATCCGGAGAGCCACACAGAGAGGCTCTTACTCTGTCA 120
DB 737 CCGTGAAGGGGCTTCTCTCATCCGGAGAGCCACACAGAGAGGCTCTTACTCTGTCA 796
QY 121 GTCCGCTCAGCCGCTTGATCTTGAGACCGGATCAGACACTACAGATCCACTGCTT 180
DB 400 GTCCGCTCAGCCGCTTGATCTTGAGACCGGATCAGACACTACAGATCCACTGCTT 459
QY 181 GACAAATGGCTGCTGTAATCTTCAACCGCGCTCACTTCCCTCACTCCAGGCGCTGTG 240
DB 460 GACAAATGGCTGCTGTAATCTTCAACCGCGCTCACTTCCCTCACTCCAGGCGCTGTG 519
QY 241 GACCAATTAC 249
DB 520 GACCAATTAC 528

RESULT 5
AX443135/c
LOCUS      AX443135      1183 bp      DNA      linear      PAT 02-JUL-2002
DEFINITION      Sequence 76 from Patent WO0216599.
ACCESSION      AX443135
VERSION      AX443135.1 GI:21690556
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1
AUTHORS      Burgess,C.E., Conley,P.B., Grose,W.M., Hart,M., Kekuda,R.,
Shinkes,R.A., Spytek,K.A., Szekeres,E.S., Tomlinson,J.E.,
Topper,J.N. and Yang,R.B.
TITLE      Proteins and nucleic acids encoding same
JOURNAL      Patent: WO 0216599-A 76 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
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Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTGATGAGGAGGCTTGAGCAGAGGAGAAAGCAGAGAACTGCTGTTGTTACTGGGAAC 60
DB 507 TGGCTGATGAGGAGGCTTGAGCAGAGGAGAAAGCAGAGAACTGCTGTTGTTACTGGGAAC 448
QY 61 CCGTGAAGGGGCTTCTCTCATCCGGAGAGCCACACAGAGAGGCTCTTACTCTGTCA 120
DB 447 CCGTGAAGGGGCTTCTCTCATCCGGAGAGCCACACAGAGAGGCTCTTACTCTGTCA 388
QY 121 GTCCGCTCAGCCGCTTGATCTTGAGACCGGATCAGACACTACAGATCCACTGCTT 180
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QY 181 GACAAATGGCTGCTGTAATCTTCAACCGCGCTCACTTCCCTCACTCCAGGCGCTGTG 240
DB 327 GACAAATGGCTGCTGTAATCTTCAACCGCGCTCACTTCCCTCACTCCAGGCGCTGTG 268
QY 241 GACCAATTAC 249
DB 267 GACCAATTAC 259

RESULT 6
AK025645
LOCUS      AK025645      2415 bp      mRNA      linear      PRI 29-SEP-2000
DEFINITION      Homo sapiens cDNA: FLJ21992 fls, clone HBP06554.
ACCESSION      AK025645
VERSION      AK025645.1 GI:10438227
KEYWORDS      oligo capping; fls (full insert sequence).
SOURCE      Homo sapiens hepatoma cell_line:hep62 cDNA to mRNA, clone_1lb:HBP
clone:HBP06554.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

REFERENCE 1 (sites)
 AUTHORS Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y.,
 Okamoto, S., Ohtani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
 Shidhara, T., Tanaka, T., Nakamura, Y., Isegai, T. and Sugano, S.
 TITLE MEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2415)
 AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isegai, T.,
 Shidhara, T., Tanaka, T. and Nakamura, Y.
 TITLE Direct Submission
 JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure Analysis, Human
 Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
 Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)
 COMMENT MEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction: 5' - & 3' - end one pass sequencing; Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by science and Technology
 Agency).

FEATURES
 source Location/Qualifiers
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 KAEELLPLGNPGAFILRESGRTGYSLSVRSRPSMDIRHRYRHCIDNGLMIYI
 SPRLTPSLQALVDHYSELADICCLIKRCPQORAGLPKXDIPLPYVQRTPLNMK
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CDS
 599 a 662 c 618 g 536 t

BASE COUNT
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Query Match 100.0%; Score 249; DB 9; Length 2415;
 Best Local Similarity 100.0%; Pred. No. 1.2e-58;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTGTATGAGGCGCTGAGCAGGAGAAAGCAGGAACTGCTGTGTTACCTGGGAAAC 60
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 DB 400 CCGAGAGGGGCGCTTCTCATCTCGGAGAGCCAGACAGAGAGGCTCTTACTCTGTCA 459
 QY 121 GTCCGCTCAGCGCGCCGATCCTGAGACCGGATCGACATCAGATCCACTGCTT 180
 DB 460 GTCCGCTCAGCGCGCCGATCCTGAGACCGGATCGACATCAGATCCACTGCTT 519
 QY 181 GACAAATGCTGGCTGTACATCTCAGCGGCTCCTTCCCTCACTCCAGGCCCTGTG 240
 DB 520 GACAAATGCTGGCTGTACATCTCAGCGGCTCCTTCCCTCACTCCAGGCCCTGTG 579
 QY 241 GACCAATTAC 249
 DB 580 GACCAATTAC 588

RESULT 7
 AX452880
 LOCUS
 DEFINITION Sequence 1 from Patent WO0242457.

2567 bp DNA linear PAT 06-JUL-2002

ACCESSION AX452880
 VERSION AX452880.1 GI:21712520
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Chang, H., Yang, W.P., Wu, Y., Whitney, G.S., Perez-Villar, J.J. and
 Kanner, S.B.
 TITLE Cloning and expression of human slap-2: a novel sh2/sh3
 domain-containing human slap homologue having immune cell-specific
 expression
 JOURNAL Patent: WO 0242457-A 1 30-MAY-2002;
 Bristol-Myers Squibb Co. (US)

FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:9606"

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 Best Local Similarity 100.0%; Pred. No. 1.2e-58;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTGTATGAGGCGCTGAGCAGGAGAAAGCAGGAACTGCTGTGTTACCTGGGAAAC 60
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 DB 754 CCGAGAGGGGCGCTTCTCATCTCGGAGAGCCAGACAGAGAGGCTCTTACTCTGTCA 813
 QY 121 GTCCGCTCAGCGCGCCGATCCTGAGACCGGATCGACATCAGATCCACTGCTT 180
 DB 814 GTCCGCTCAGCGCGCCGATCCTGAGACCGGATCGACATCAGATCCACTGCTT 873
 QY 181 GACAAATGCTGGCTGTACATCTCAGCGGCTCCTTCCCTCACTCCAGGCCCTGTG 240
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 QY 241 GACCAATTAC 249
 DB 934 GACCAATTAC 942

RESULT 8
 AF287467
 LOCUS AF287467 1348 bp mRNA linear ROD 03-JUN-2002
 DEFINITION Mus musculus Src-1-like adaptor protein-2 mRNA, complete cds.
 ACCESSION AF287467
 VERSION AF287467.1 GI:17351918
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Loreto, M.P., Berry, D.M. and McGlade, C.J.
 TITLE Functional cooperation between c-Cbl and Src-1-like adaptor protein 2
 in the negative regulation of T-cell receptor signaling
 JOURNAL Mol. Cell. Biol. 22 (12), 4241-4255 (2002)
 MEDLINE 22022020
 PUBMED 12024036

REFERENCE 2 (bases 1 to 1348)
 AUTHORS Loreto, M.P. and McGlade, C.J.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2000) Brain Tumour Research Centre, Hospital for
 Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

FEATURES
 source Location/Qualifiers
 1..1348
 /organism="Mus musculus"

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WormPEP; information on the WormPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>

This sequence is the entire insert of clone RPS-977B1. The true left end of clone RPS-977B1 is at 63245 in this sequence. The true right end of clone RPS-977B1 is at 63218 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPS-977B1 is from the library RPS-5 constructed by the group of Pieter de Jong. For further details see <http://www.choi.org/bacpac/home.htm>

VECTOR: pCYPAC2.

FEATURES

SOURCE

Location/Qualifiers

1. 145068

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/db_xref="taxon:9606"

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/clone_1b="RPS-5"

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/note="match: GSS: Em:AQ620498"

1047..1629

/note="match: GSS: Em:AQ79162"

1631..1923

/note="AluSx repeat: matches 1..294 of consensus"

2776..2842

/note="L2 repeat: matches 2357..2423 of consensus"

3891..3949

/note="MIR repeat: matches 34..90 of consensus"

4458..4611

/note="MIR repeat: matches 67..231 of consensus"

5133..5549

/note="L1M2 repeat: matches 5924..6340 of consensus"

5550..5680

/note="F1M1_C repeat: matches 1..132 of consensus"

5703..5890

/note="AluSq repeat: matches 120..308 of consensus"

5923..6012

/note="L1M2 repeat: matches 5432..5528 of consensus"

6588..6889

/note="AluSx repeat: matches 1..303 of consensus"

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/evidence="not experimental"

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1631..1923

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Matches 165; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 120 AGTCGGCTTACGCCCTGCTGATCTCTGGAGCCGATCAGACATCAAGATCCATCTGCT 179
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Db 125956 GGACCATTAC 125947

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DEFINITION      Homo sapiens chromosome 20 clone RP11-712N14 map 20, WORKING DRAFT
SEQUENCE      37 unordered pieces.
ACCESSION      AC026539.2 GI:7656813
VERSION      HTG: HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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1 (bases 1 to 145833)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome 20, clone RP11-712N14
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 145833)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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TITLE JOURNAL COMMENT

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Klein,J., Labèque,K., Lamazares,R., Landers,T., Lebecky,J.,
Levine,R., Lien,C., Liu,G., Locke,K., MacDonald,P., Margus,N.,
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Stange-Thomann,N., Stojanovic,N., Subramanian,A., Tajamas,J.,
Tessier,S., Theodore,J., Tittel,A., Travers,M., Trisillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 27, 2000 this sequence version replaced gi:7283243.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7115
Center clone name: 712_N_14
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960721
Consensus quality: 125577 bases at least Q40
Consensus quality: 135703 bases at least Q40
Consensus quality: 139593 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 142233; sum-of-contigs
Quality coverage: 2.6 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1315 1314: gap of 100 bp
1315 2673: contig of 1359 bp in length
2674 2773: gap of 100 bp
2774 4520: contig of 1747 bp in length
4521 4620: gap of 100 bp
4621 5961: contig of 1341 bp in length
5962 6061: gap of 100 bp
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21103 21202: gap of 100 bp
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Best Local Similarity 86.8%; Score 150; DB 2; Length 145833;
Matches 165; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 120 AGTCCGCTCAGCCGCGCTGATCTCTGGAGCCGATCAGACATCAGATTCACGCGCT 179
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Qy 180 TGACATGCTGCTGATCATCTCAGCGGCTCAGCTTCCCTTACTCTCAGGCGCTGCT 239
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Qy 240 GGACCATTCAC 249
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RESULT 12

AC125701

LOCUS

DEFINITION

AC125701

VERSION

AC125701.3

KEYWORDS

HTG; HTGS; PHASE1.

SOURCE

ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine;

Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 168498)
 Murthy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Albrooke,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,


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Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
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Weinstock G., and Gibbs R.

Direct Submission
Unpublished
2 (bases 1 to 168498)
Worley K.C.
Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168498)
Worley K.C.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Project Information
Center project name: GDYR
Center clone name: CH230-12U23
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Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 126947 bases at least Q40
Consensus quality: 134611 bases at least Q30
Consensus quality: 140704 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

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* be preserved.
1 1011: contig of 1011 bp in length

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* 7099 7198: gap of unknown length
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* 8633 8732: gap of unknown length
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* 25481 26540: contig of 1060 bp in length
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TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 114096)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 114096)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Jul 19, 2002 this sequence version replaced gi:21281284.
 ----- Genome Center
 Center: Baylor College of Medicine

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LOCUS				
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ACCESSION	AC123560			
VERSION	AC123560.2	GI:21908372		
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AUTHORS	Muzny,D.M., Adams,C., Aiso-Otsubo,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayala,M., Banks,T.,			

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Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 114096)
Morley, K.C.

Direct Submission
Submitted (31-MY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 114096)
Morley, K.C.

Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 19, 2002 this sequence version replaced gi:21281284.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXON
Center clone name: CH230-61G22
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 92427 bases at least Q40
Consensus quality: 95724 bases at least Q30
Consensus quality: 98040 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_difft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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* 49611: gap of unknown length
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* 57185: contig of 4477 bp in length
* 61662: gap of unknown length
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* 69639: gap of unknown length
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* 81837: gap of unknown length
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FEATURES

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 /clone="CH230-61G22"
 BASE COUNT 28756 a 25752 c 25413 g 28712 t 5463 others
 ORIGIN

Query Match 49.2%; Score 122.6; DB 2; Length 114096;
 Best Local Similarity 77.2%; Pred. No. 1.1e-23;
 Matches 149; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 116 TGTCAATCCGCTTACAGCCGCTTGACCTTGGAGACCGAGTAACTACAGACTCACT 175
Db 18258 TGTCAATCCGCTTACAGCCGCTTGACCTTGGAGACCGAGTAACTACAGACTCACT 18317
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RESULT 14

AC026539

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

TITLES

AUTHORS

JOURNAL

REFERENCE

AUTHORS

TITLES

JOURNAL

REFERENCE

AUTHORS

TITLES

JOURNAL

REFERENCE

AUTHORS

TITLES

JOURNAL

REFERENCE

AC026539 145833 bp DNA linear HTG 27-APR-2000
 Homo sapiens chromosome 20 clone RP11-712M14 map 20, WORKING DRAFT
 SQUENCE, 37 unordered pieces.
 AC026539
 HTG: HTGS PHASE1; HTGS_DRAFT.
 Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 145833)
 Birren, B., Linton, L., Nuebaum, C. and Lander, E.
 Homo sapiens chromosome 20, clone RP11-712M14
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 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submissions
 Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 27, 2000 this sequence version replaced gi:1283243.
 All repeats were identified using RepeatMasker:
 Smit, A. F. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center

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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L7115
Center clone name: 712 N 14
----- Summary Statistics -----
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 125577 bases at least Q40
Consensus quality: 135703 bases at least Q30
Consensus quality: 139593 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 142233; sum-of-contigs
Quality coverage: 2.6 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1215 1314: gap of 100 bp
* 1315 2673: contig of 1359 bp in length
* 2674 2773: gap of 100 bp
* 2774 4520: contig of 1747 bp in length
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* 6062 7719: contig of 1658 bp in length
* 7720 7819: gap of 100 bp
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